

SEQUENCE LISTING

<110> Mahajan, Pramod B.
Shi, Jinrui

<120> Maize Rad50 Orthologue and Uses Thereof

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Thr	Val	Asp	Lys	Met	Leu	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Asp	Pro	Asp	
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aat	aag	aac	gtc	atc	acc	ttc	ttc	aag	ccg	ctc	acc	ctc	atc	gtt	ggc	393
Asn	Lys	Asn	Val	Ile	Thr	Phe	Phe	Lys	Pro	Leu	Thr	Leu	Ile	Val	Gly	
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ccc	aac	ggt	gct	ggc	aag	acc	acg	atc	atc	gag	tgc	ctg	aag	ctt	tct	441
Pro	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Ile	Ile	Glu	Cys	Leu	Lys	Leu	Ser	
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Cys	Thr	Gly	Glu	Leu	Pro	Pro	Asn	Ser	Arg	Ser	Gly	His	Thr	Phe	Val
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His	Asp	Pro	Lys	Val	Ala	Gly	Glu	Thr	Glu	Thr	Lys	Gly	Gln	Ile	Lys	
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ttg	cgg	ttt	aag	act	gca	gca	gga	aag	gat	gtg	gtg	tgc	atc	cgg	tcc	585
Leu	Arg	Phe	Lys	Thr	Ala	Ala	Gly	Lys	Asp	Val	Val	Cys	Ile	Arg	Ser	
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tcc aat tgg cca ttg cag gac ccg tca aca ctt aag aag aag ttc gat Ser Asn Trp Pro Leu Gln Asp Pro Ser Thr Leu Lys Lys Lys Phe Asp			825
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gac atc ttc tct gcc aca cgc tat acg aaa gct ctt gaa gtc ata aag Asp Ile Phe Ser Ala Thr Arg Tyr Thr Lys Ala Leu Glu Val Ile Lys			873
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260	265		270
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275	280	285	290
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gaa tgg caa aca aaa ttt gaa gaa agg att gcg tta cta gaa aca aaa Glu Trp Gln Thr Lys Phe Glu Glu Arg Ile Ala Leu Leu Glu Thr Lys			1257
310	315		320
atc agt aaa ctt gta aga gat atg gat gat gaa gca tct tat agc tcc Ile Ser Lys Leu Val Arg Asp Met Asp Asp Glu Ala Ser Tyr Ser Ser			1305
325	330		335
gtt ctg tcc aaa caa aat tct gaa tta aca cat gaa att gga aag ctc Val Leu Ser Lys Gln Asn Ser Glu Leu Thr His Glu Ile Gly Lys Leu			1353
340	345		350

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cat ccc ttt acg aat gat gtt gct atg aac ctt aca aac agg att aaa His Pro Phe Thr Asn Asp Val Ala Met Asn Leu Thr Asn Arg Ile Lys 390 395 400	1497
gcg aga cta tca agt ctt gag aat gat ttg ctg gat aag aag aaa tcc Ala Arg Leu Ser Ser Leu Glu Asn Asp Leu Leu Asp Lys Lys Lys Ser 405 410 415	1545
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gct gca gaa gtg gag ctt tca aaa ttt aat cta tcc cgt atc gat gag Ala Ala Glu Val Glu Leu Ser Lys Phe Asn Leu Ser Arg Ile Asp Glu 470 475 480	1737
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 Leu Ser Cys Thr Gly Glu Leu Pro Pro Asn Ser Arg Ser Gly His Thr
 50 55 60
 Phe Val His Asp Pro Lys Val Ala Gly Glu Thr Glu Thr Lys Gly Gln
 65 70 75 80
 Ile Lys Leu Arg Phe Lys Thr Ala Ala Gly Lys Asp Val Val Cys Ile
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 Arg Ser Phe Gln Leu Thr Gln Lys Ala Ser Lys Met Glu Phe Lys Ala
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 Ile Glu Ser Val Leu Gln Thr Ile Asn Pro His Thr Gly Glu Lys Val
 115 120 125
 Cys Leu Ser Tyr Arg Cys Ala Asp Met Asp Arg Glu Ile Pro Ala Leu
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 Met Gly Val Ser Lys Ala Val Leu Glu Asn Val Ile Phe Val His Gln
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 Asp Glu Ser Asn Trp Pro Leu Gln Asp Pro Ser Thr Leu Lys Lys Lys
 165 170 175
 Phe Asp Asp Ile Phe Ser Ala Thr Arg Tyr Thr Lys Ala Leu Glu Val
 180 185 190
 Ile Lys Lys Leu His Lys Asp Gln Met Gln Glu Ile Lys Thr Phe Arg
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 Leu Lys Leu Glu Asn Leu Gln Thr Val Lys Asp Gln Ala His Lys Leu
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 Arg Glu Asn Ile Ala Gln Asp Gln Glu Lys Ser Asp Ala Ser Lys Ser
 225 230 235 240
 Gln Met Glu Gln Leu Lys Glu Lys Ile Cys Gly Thr Glu Arg Glu Ile
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 Ile Asp Ile Lys Ala Thr Glu Arg Ser Thr Leu Leu Thr Gln Gln His
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 Glu Lys Leu Ala Ala Leu Ser Glu Glu Asn Glu Asp Thr Asp Glu Glu
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 Thr Lys Ile Ser Lys Leu Val Arg Asp Met Asp Asp Glu Ala Ser Tyr
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 Ser Ser Val Leu Ser Lys Gln Asn Ser Glu Leu Thr His Glu Ile Gly
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 Lys Leu Gln Ala Glu Ala Asp Ala His Leu Thr Met Lys His Glu Arg
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 Asp Ser Asp Ile Lys Asn Ile Cys Thr Lys His Asn Leu Gly Pro Val
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 Pro Glu His Pro Phe Thr Asn Asp Val Ala Met Asn Leu Thr Asn Arg
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Asp	Glu	Arg	Glu	Arg	His	Met	Gln	Ile	Glu	Val	Glu	Arg	Lys	Thr	Leu
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Ala	Leu	Gly	Glu	Arg	Asp	Tyr	Asp	Ser	Ile	Ile	Ser	Gln	Lys	Arg	Thr
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Glu	Val	Tyr	Ser	Leu	Glu	Gln	Lys	Ile	Lys	Val	Leu	Leu	Arg	Glu	Lys
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Asp	Ile	Ile	Asn	Arg	Asn	Ala	Asp	Glu	Arg	Val	Lys	Leu	Gly	Leu	Lys
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Lys	Asp	Ala	Leu	Glu	Ser	Ser	Lys	Asp	Lys	Leu	Asn	Glu	Ile	Val	Asn
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Glu	His	Lys	Asp	Lys	Ile	Lys	Lys	Val	Leu	Arg	Gly	Arg	Asn	Pro	Phe
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Lys	Glu	Tyr	Asn	Glu	Leu	Arg	Ser	Lys	Ser	Gln	Glu	Ala	Glu	Gln	Glu
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Leu	Lys	Phe	Thr	Gln	Ser	Lys	Val	Thr	Asp	Ala	Arg	Glu	Gln	Leu	Thr
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Lys	Leu	Arg	Arg	Asp	Met	Asp	Ala	Lys	Arg	Arg	Phe	Leu	Asp	Ser	Lys
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Leu	Gln	Ser	Ile	Leu	Gln	Ile	Ser	Ala	Asn	Val	Asp	Met	Phe	Pro	Lys
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Ala	Arg	Lys	Asn	His	Val	Cys	Pro	Cys	Cys	Glu	Arg	Ala	Phe	Thr	Pro
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Asp	Glu	Glu	Asp	Glu	Phe	Val	Lys	Lys	Gln	Arg	Met	Gln	Asn	Ser	Ser
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Thr	Ala	Glu	Arg	Ser	Lys	Ala	Leu	Ala	Met	Glu	Ser	Ser	Asn	Ala	Glu
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Ala	Leu	Phe	Gln	Gln	Leu	Asp	Lys	Leu	Arg	Thr	Ile	Tyr	Asp	Ala	Tyr
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Val	Lys	Leu	Val	Glu	Glu	Thr	Ile	Pro	Leu	Ala	Glu	Lys	Asn	Leu	Asn
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Leu	Leu	Gln	Pro	Thr	Asp	Thr	Ile	Asp	Arg	His	Val	His	Glu	Ile	Gln
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Gln	Leu	Val	Lys	Glu	Val	Glu	Asp	Leu	Glu	Tyr	Ala	Leu	Asp	Ser	Ser
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Gly	Arg	Gly	Val	Lys	Ser	Leu	Glu	Glu	Ile	Gln	Leu	Glu	Leu	Asn	Phe
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Asp	Gln	His	Arg	Met	Leu	Asn	Glu	Asp	Met	Ser	Ser	Ala	Gln	Val	Arg
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Trp	His	Asn	Ala	Arg	Glu	Glu	Lys	Val	Lys	Ala	Ser	Ser	Ile	Leu	Glu
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Arg	Phe	Gln	Lys	Ser	Glu	Glu	Glu	Leu	Val	Leu	Leu	Ala	Glu	Glu	Lys
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Glu	Gln	Leu	Ile	Val	Glu	Lys	Lys	Leu	Leu	Glu	Glu	Ser	Leu	Asp	Pro
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Leu	Ser	Lys	Glu	Ser	Leu	Leu	Gln	Glu	Tyr	Asn	Ala	Leu	Lys		

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Gln	Lys	Leu	Asp	Glu	Glu	Tyr	His	Gln	Leu	Ala	Glu	Arg	Lys	Arg	Glu
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Phe	Gln	Glu	Leu	Asp	Ala	Leu	Gly	Arg	Leu	Asn	Met	Lys	Ile	Lys	
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Gly	Tyr	Leu	Asp	Ser	Lys	Lys	Asn	Glu	Lys	Leu	Lys	Glu	Leu	Gln	Gly
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Arg	His	Val	Leu	Cys	His	Ser	Gln	Leu	Gln	Ser	Cys	Met	Ala	Lys	Gln
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Gln	Arg	Ile	Ser	Ala	Glu	Leu	Asn	Lys	Ser	Lys	Glu	Leu	Leu	Gln	Gly
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Thr	Lys	Ala	Asp	Val	Glu	Gln	Leu	Thr	Arg	Asp	Ile	Glu	Ser	Leu	Glu
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Glu	Arg	Leu	Leu	Ser	Ile	Gly	Ser	Leu	Ser	Ala	Ile	Glu	Ala	Asp	Leu
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Lys	Arg	His	Ser	Gln	Glu	Lys	Glu	Arg	Leu	Asn	Ser	Glu	Phe	Asn	Arg
				1075				1080							1085
Trp	Gln	Gly	Thr	Leu	Ser	Val	Tyr	Gln	Ser	Asn	Ile	Ser	Lys	His	Lys
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Gln	Glu	Leu	Lys	Leu	Ser	Gln	Tyr	Lys	Asp	Ile	Glu	Lys	Arg	Tyr	Thr
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Asp	Arg	Tyr	Tyr	Thr	Ala	Leu	Asp	Lys	Ala	Leu	Met	Arg	Phe	His	Ser
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Met	Lys	Met	Glu	Glu	Ile	Asn	Lys	Ile	Ile	Lys	Glu	Leu	Trp	Gln	Gln
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Thr	Tyr	Arg	Gly	Gln	Asp	Ile	Asp	Tyr	Ile	Ser	Ile	Asn	Ser	Asp	Ser
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Glu	Gly	Ala	Gly	Thr	Arg	Ser	Tyr	Ser	Tyr	Arg	Val	Val	Met	Gln	Thr
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Gly	Pro	Asn	Ala	Glu	Ser	Leu	Ala	Ala	Leu	Leu	Arg	Ile	Met	Glu	
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Tyr	Arg	Val	Ser	Lys	Asp	Glu	Asn	Gln	His	Ser	Ile	Ile	Glu	Ser	Gln
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<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide based upon an adaptor used for cDNA library construction and poly(dT) to remove clones which have a poly(A) tail but no cDNA insert.

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36

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